Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 04:32:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038429.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR5038429 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038429_1.fastq.gz SRR5038429_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 04:32:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038429.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,639,096
Mapped reads	17,670,287 / 94.8%
Unmapped reads	968,809 / 5.2%
Mapped paired reads	17,670,287 / 94.8%
Mapped reads, first in pair	8,939,882 / 47.96%
Mapped reads, second in pair	8,730,405 / 46.84%
Mapped reads, both in pair	17,397,032 / 93.34%
Mapped reads, singletons	273,255 / 1.47%
Secondary alignments	0
Supplementary alignments	318,466 / 1.71%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	3,783,581 / 20.3%
Duplication rate	14.79%
Clipped reads	8,765,752 / 47.03%

2.2. ACGT Content

Number/percentage of A's	673,703,760 / 28.46%
Number/percentage of C's	473,081,862 / 19.99%
Number/percentage of T's	685,859,330 / 28.97%
Number/percentage of G's	534,251,602 / 22.57%
Number/percentage of N's	186,582 / 0.01%

GC Percentage	42.56%

2.3. Coverage

Mean	0.7652
Standard Deviation	10.504

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	75,643.09
Standard Deviation	2,620,104.01
P25/Median/P75	187 / 234 / 295

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	30,536,999
Insertions	454,863
Mapped reads with at least one insertion	2.42%
Deletions	849,130
Mapped reads with at least one deletion	4.61%
Homopolymer indels	46.47%

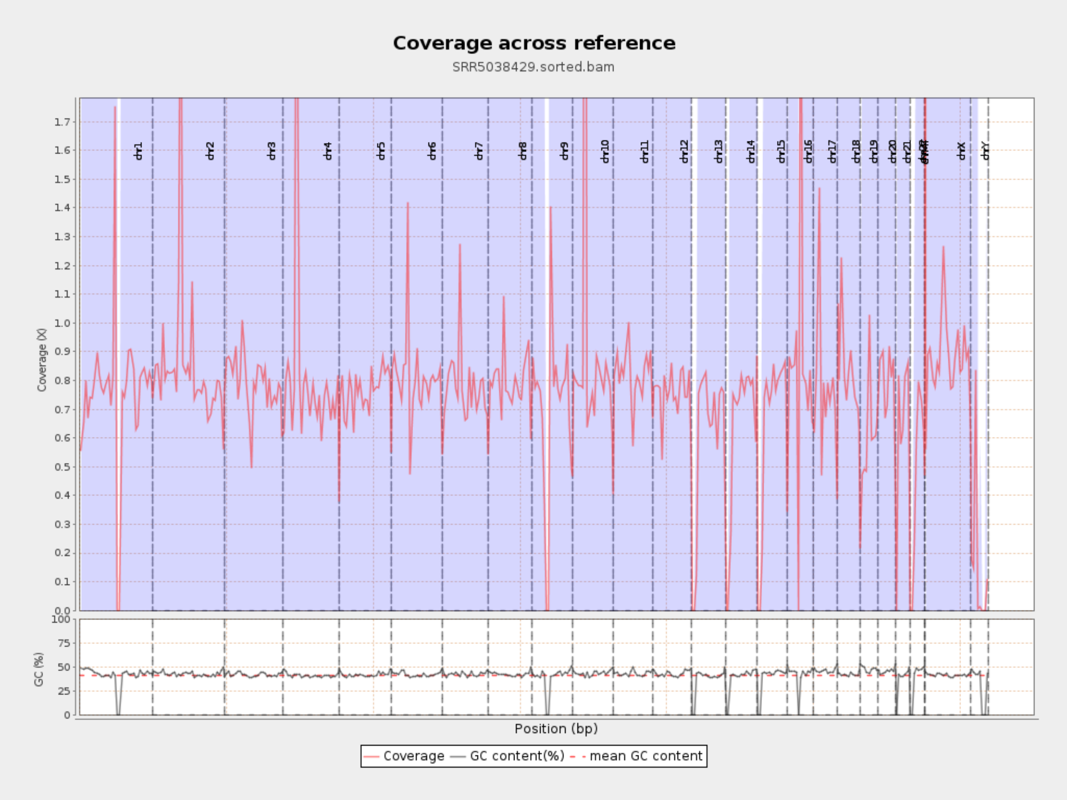
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

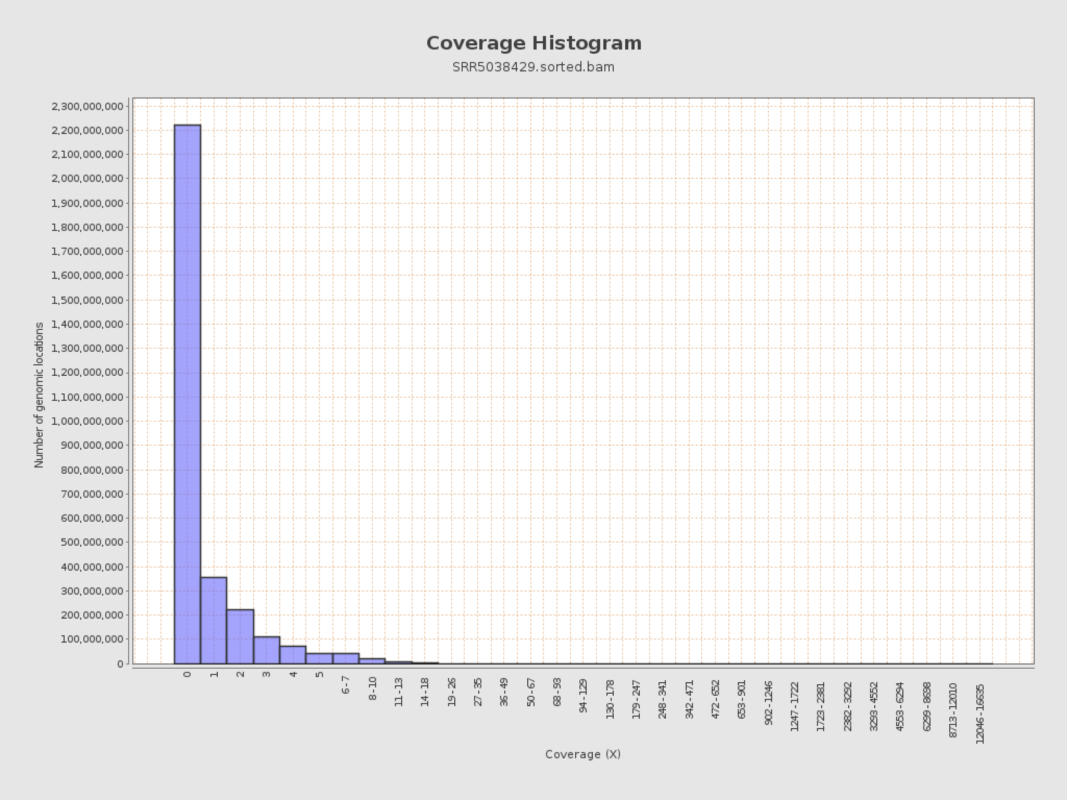
		bases	**coverage**	**deviation**
chr1	249250621	188641274	0.7568	16.6195
chr2	243199373	210463228	0.8654	11.4293
chr3	198022430	157376401	0.7947	1.7587
chr4	191154276	155261448	0.8122	12.5858
chr5	180915260	138183633	0.7638	1.7119
chr6	171115067	139587752	0.8158	7.2704
chr7	159138663	123774567	0.7778	9.6956
chr8	146364022	116796293	0.798	3.5328
chr9	141213431	97486445	0.6903	16.4374
chr10	135534747	129904423	0.9585	23.9853
chr11	135006516	110044936	0.8151	6.5316
chr12	133851895	101466337	0.758	1.8093
chr13	115169878	69699224	0.6052	1.4754
chr14	107349540	67322030	0.6271	1.732
chr15	102531392	65611093	0.6399	1.5584
chr16	90354753	79241036	0.877	12.9165
chr17	81195210	62332486	0.7677	12.4133
chr18	78077248	65455960	0.8383	13.09
chr19	59128983	35158055	0.5946	7.6833
chr20	63025520	50285058	0.7979	4.0757
chr21	48129895	31281086	0.6499	5.6184
chr22	51304566	23818392	0.4643	1.4402
chrMT	16571	3061540	184.7529	113.9898
chrX	155270560	137103557	0.883	3.5352

chrY	59373566	9498305	0.16	13.3969

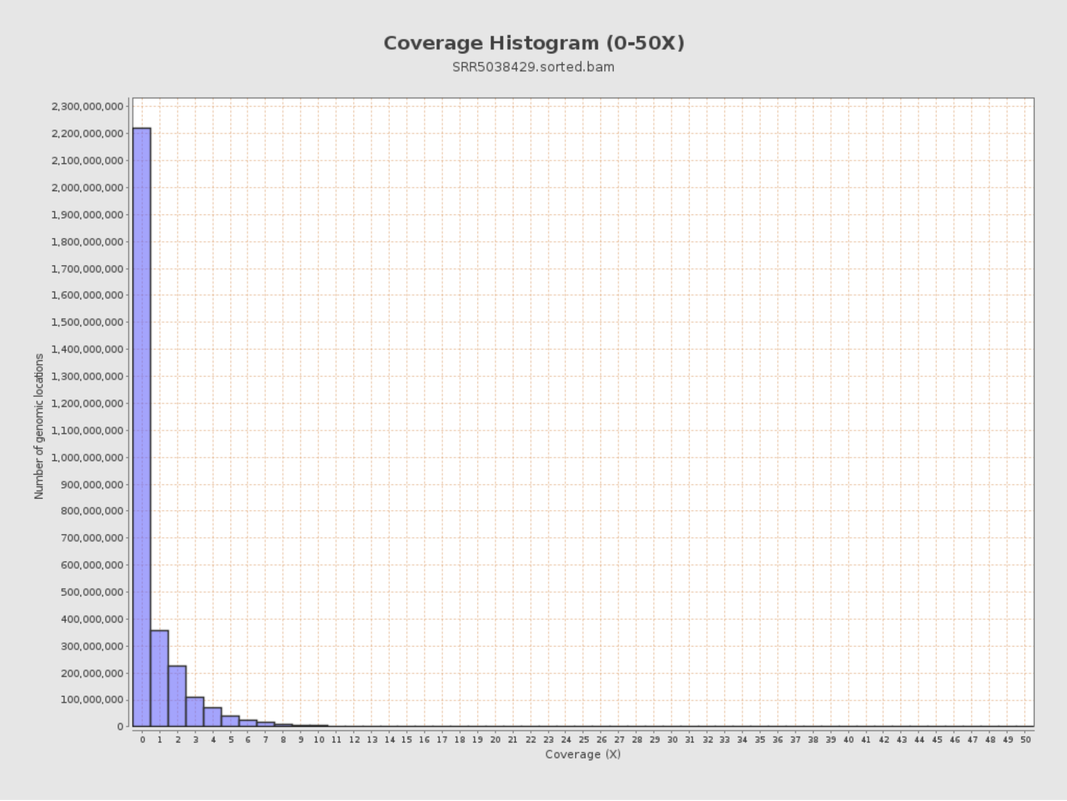
3. Results : Coverage across reference



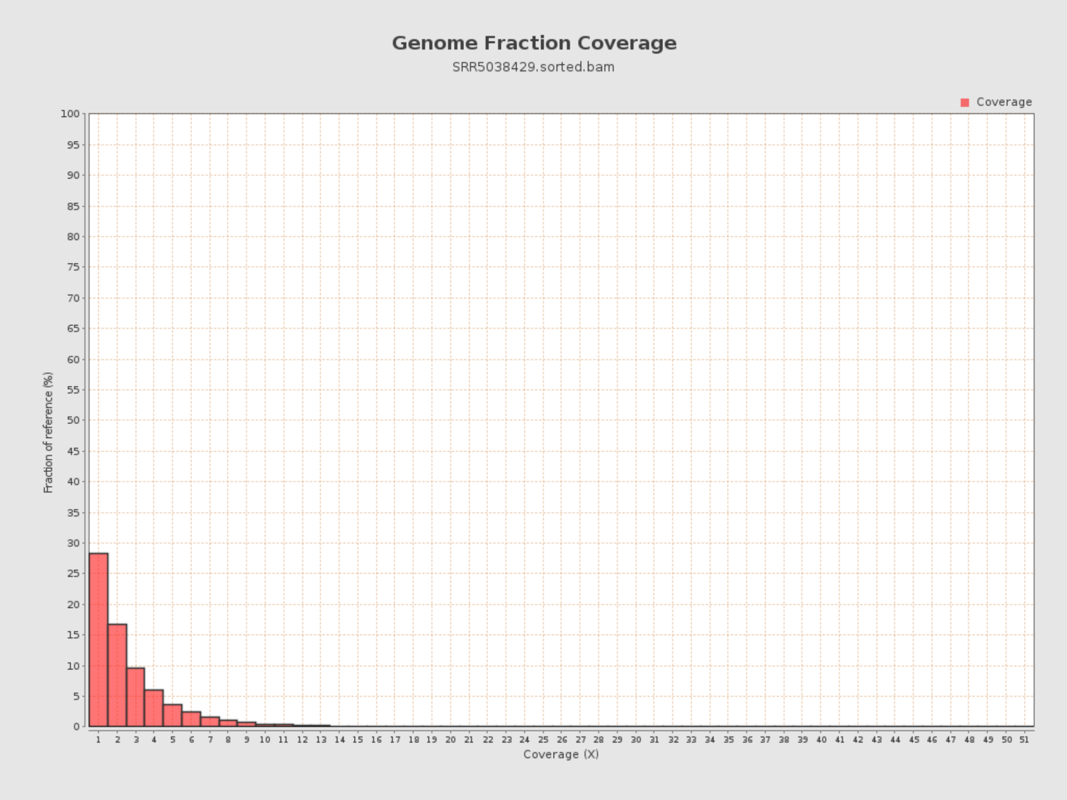
4. Results : Coverage Histogram



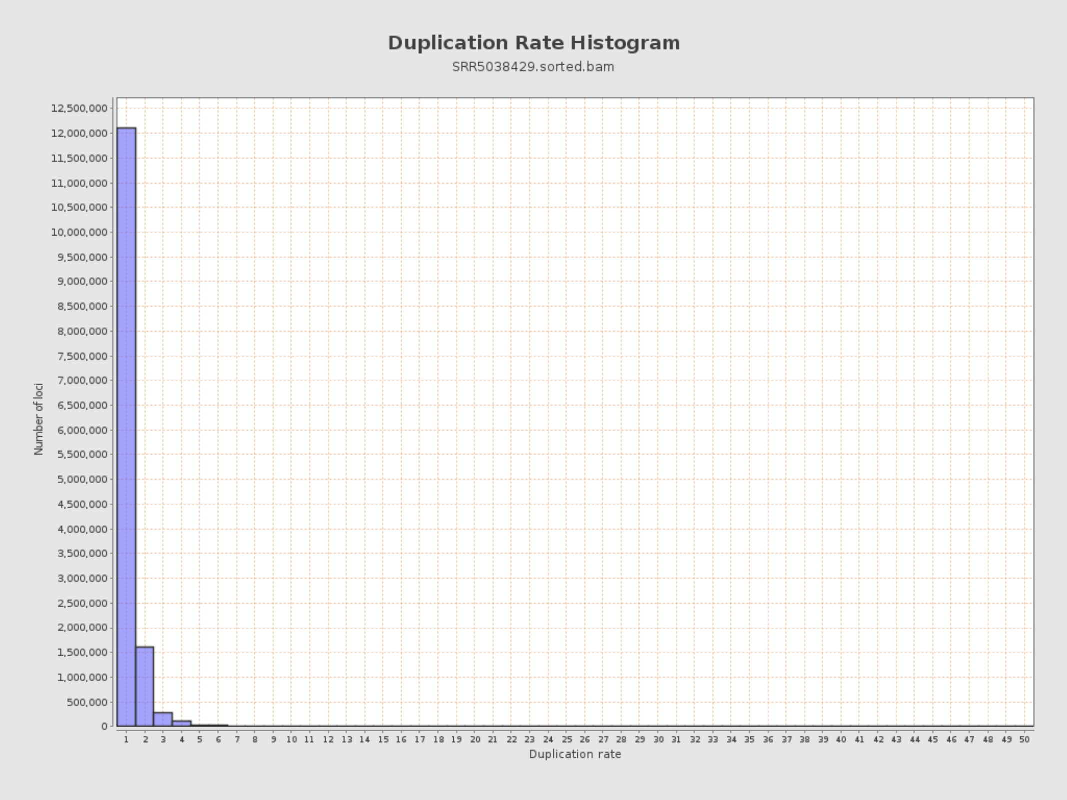
5. Results : Coverage Histogram (0-50X)



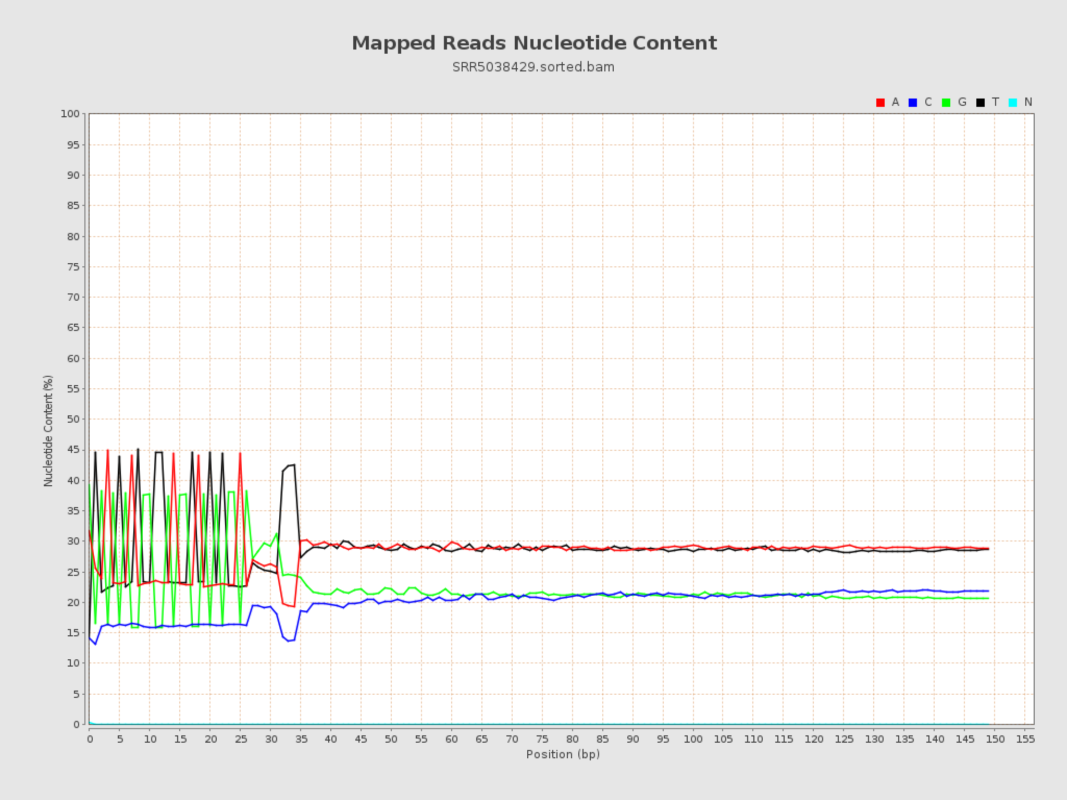
6. Results : Genome Fraction Coverage



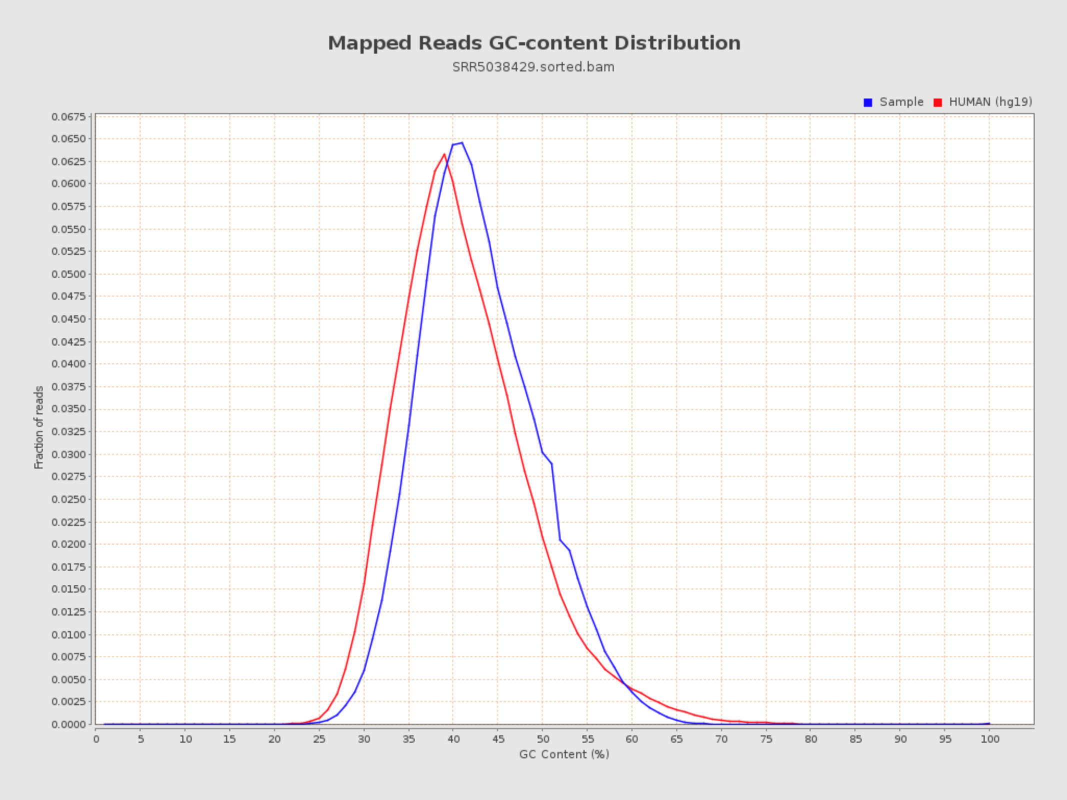
7. Results : Duplication Rate Histogram



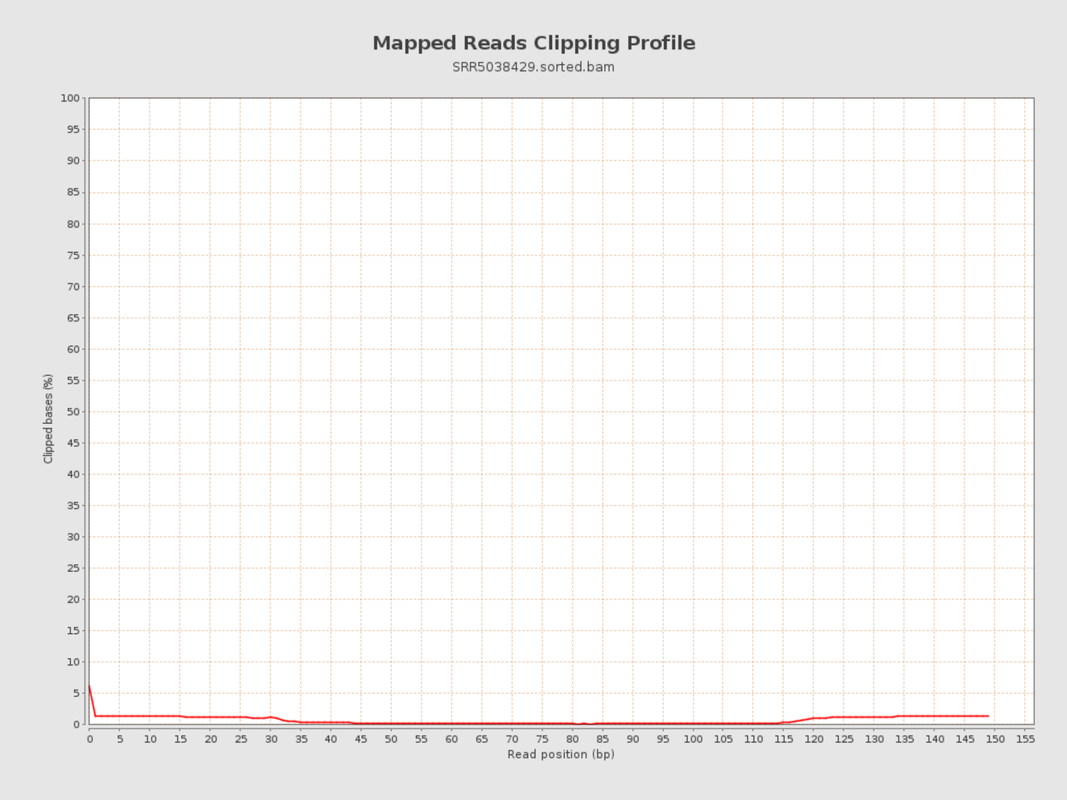
8. Results : Mapped Reads Nucleotide Content



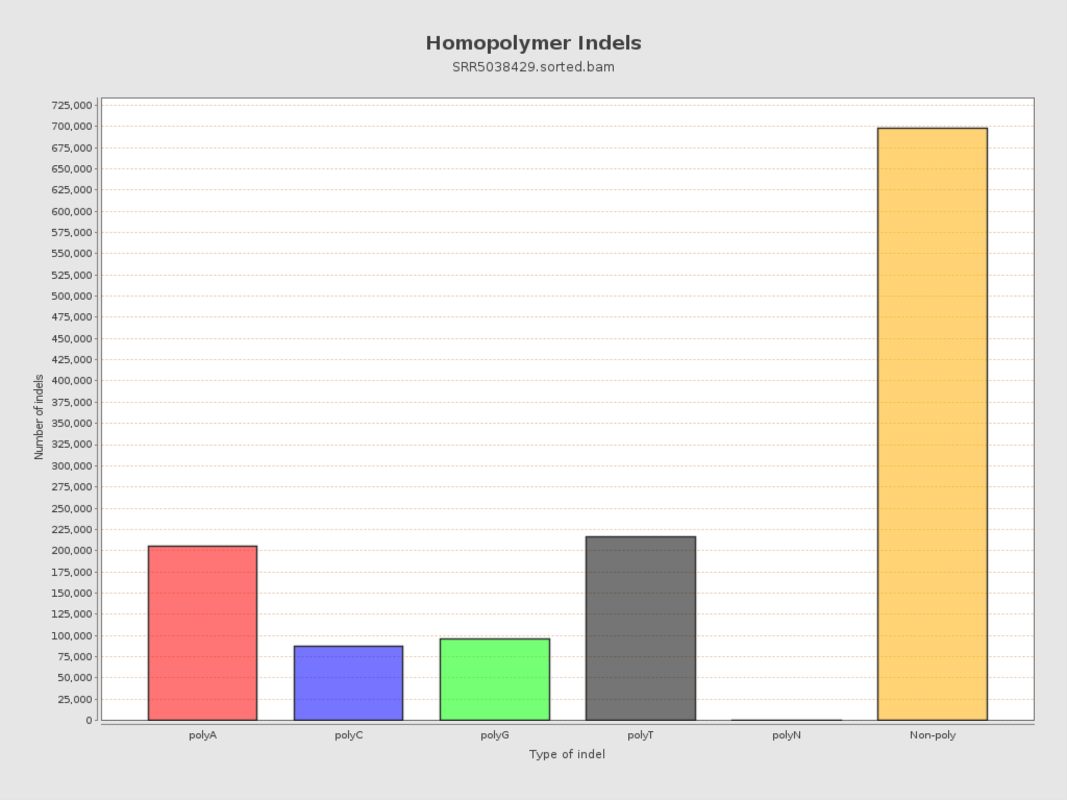
9. Results : Mapped Reads GC-content Distribution



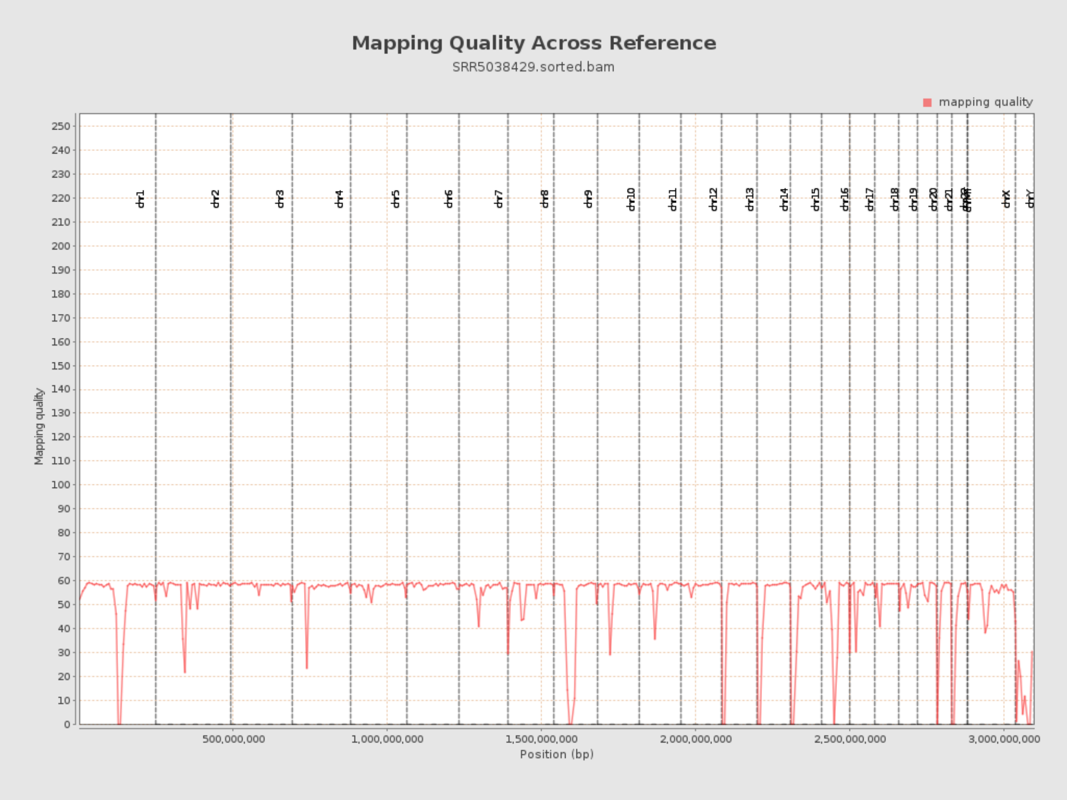
10. Results : Mapped Reads Clipping Profile



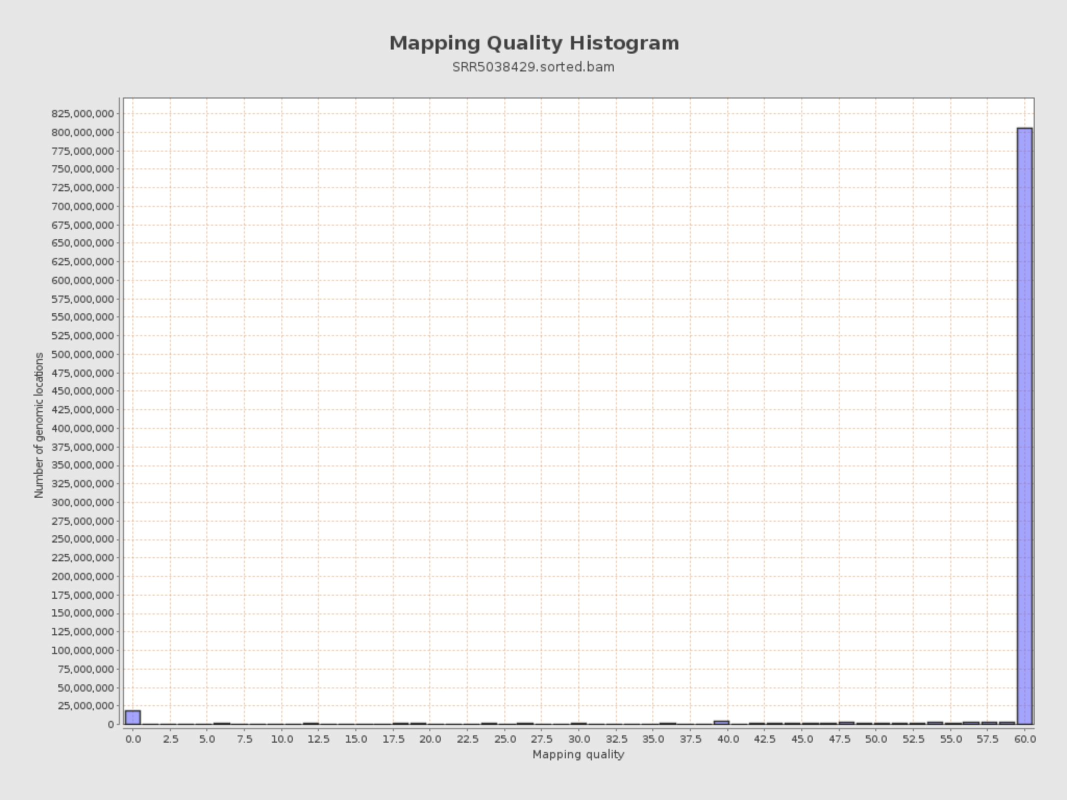
11. Results : Homopolymer Indels



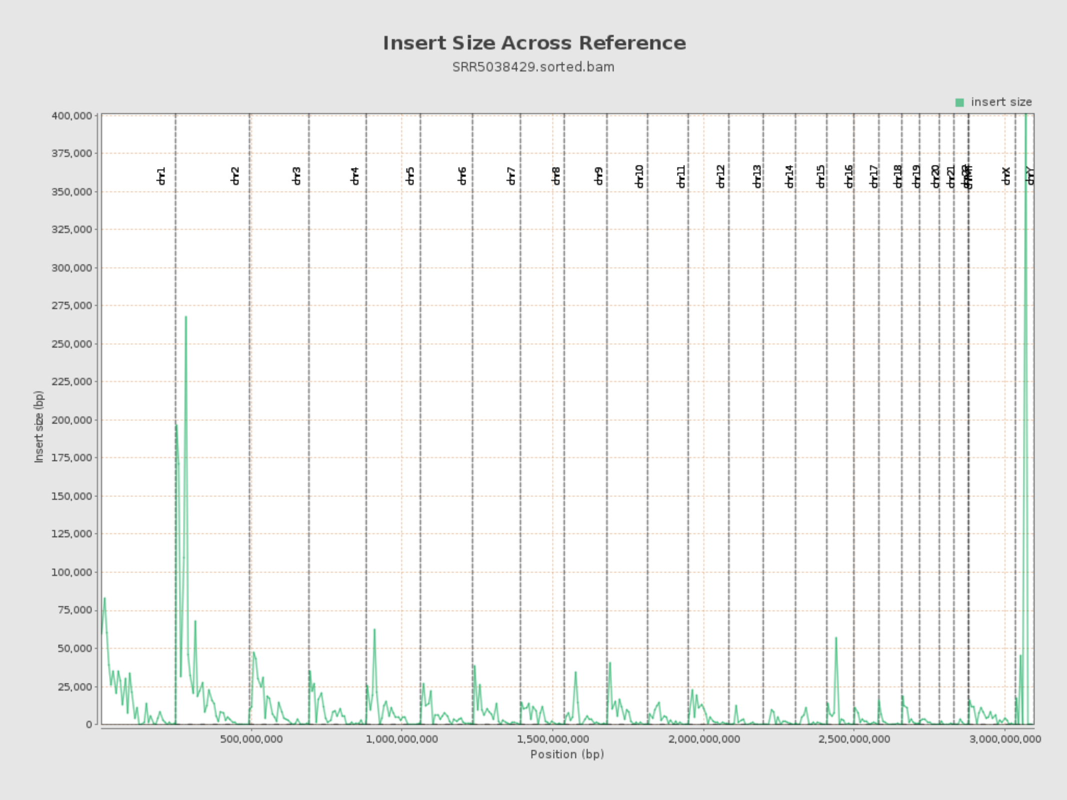
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram